Addressing the Examiner's Rejections

1. **Rejection of Claims 1-3, 5-7, 9-45 and 49-51 under 35 U.S.C. §112, Second Paragraph**

The Examiner alleged that the recitation of "at least about" in claims 1 and 5 rendered the claims indefinite. The cancellation of claim 1 renders the rejection moot. Claim 5 has been amended to recite "at least."

Claims 2, 3, and 5-7 were rejected for reciting "complements and reverse complements thereof." Claims 5-7 have been amended to recite "complement and reverse complement thereof."

Claim 5 was rejected as indefinite. The Examiner alleged it was unclear whether "50%" in part (ii) modified the sequence of SEQ ID NO:1 or the 15 contiguous nucleotides. The recitation has been deleted.

Claims 11, 12, and 24 were rejected as indefinite for reciting "control elements." The Examiner alleged that it was not clear what other elements can be considered a "control element" except for those listed on pages 20 and 21 of the specification.

The applicants traverse. Under 35 U.S.C. §112, second paragraph, the claims need only reasonably apprise a person having ordinary skill in the art as to their scope. *Hybritech Inc., v. Monoclonal Antibodies, Inc.,* 231 USPQ 81, Fed. Cir. 1986. As acknowledged by the Examiner, the applicants have exemplified "control elements" by providing typical examples throughout the specification. It is axiomatic that a patent specification "need not teach, and preferably omits, what is well known in the art." See, *Spectra-Physics, Inc. v. Coherent, Inc.*, 3 USPQ2d 1737, 1743 (Fed. Cir. 1987); *Hybritech Inc. v. Monoclonal Antibodies, Inc.*, 231 USPQ 81, 94 (Fed. Cir. 1986). The applicants have provided typical examples of control elements. Other control elements not enumerated in the specification, but recognized as such by an ordinarily skilled artisan, need not be enumerated. The applicants have defined the boundaries of the term "control elements." In view of the teachings of the specification and the level of ordinary skill in the present art, the

applicants submit that the boundaries of the term "control elements" are capable of being understood by one of ordinary skill in the art. Accordingly, applicants submit that the rejections of the claims under 35 U.S.C. §112, second paragraph, should be withdrawn.

The Examiner rejected claims 11 and 12 for the recitation "control elements operably linked to said polynucleotides." The Examiner stated that it was not clear whether the control elements referred to the once inherent in the genomic sequences or different control elements. The applicants have amended claim 12 to depend from claim 6.

The Examiner rejected claim 15 for the reciting "modulating," asserting that it was not clear if the recitation referred to increasing, decreasing, altering the activity of DWF4 polypeptide. The applicants traverse. The plain meaning of the term "modulating" encompasses the overexpression and inhibition of dwf4 expression. The applicants submit that the boundaries of the term "modulating" are capable of being understood by one of ordinary skill in the art.

The Examiner rejected claims 20-22 for recitation of "includes" alleging that it was unclear whether the term referred to open or closed language. MPEP at §2111.03 states: "The transitional term "comprising", which is synonymous with "including," "containing," or "characterized by," is inclusive or open-ended and does not exclude additional, unrecited elements or method steps." Thus, the use of the term "includes" which is synonymous with "comprises" is open-ended, and would be understood as such by one of ordinary skill in the art.

In view of the above remarks and amendments, the teachings of the specification and the level of ordinary skill in the present art, applicants submit that the boundaries of claims are capable of being understood by one of ordinary skill in the art. Accordingly, the rejections of the claims under 35 U.S.C. §112, second paragraph, should be withdrawn.

Rejection of Claims 1, 2, 4-6, and 8-51 under 35 U.S.C. §112, First Paragraph

The Examiner has rejected claims 1, 2, 4-6, and 8-51 under 35 U.S.C. §112, first paragraph, asserting that the specification does not reasonably provide written description for the claims. The Examiner states that the specification describes the isolation and sequencing of a genomic clone (SEQ ID NO:1) encoding the Arabidopsis DWF4 polypeptide (SEQ ID NO:2), but does not teach the nucleotide sequence of any other dwf4 polynucleotide, or their control elements. The Examiner states that the specification fails to provide an adequate written description for the polynucleotide sequences encompassed by the claims.

The applicants traverse. Claim 5 pertains to an isolated *dwf4* polynucleotide comprising (i) a sequence having at least 90% identity to SEQ ID NO:1, complement and reverse complement thereof or (ii) a sequence comprising at least 15 contiguous nucleotides of SEQ ID NO:1, complement and reverse complement thereof. The applicants have taught the sequence comprising SEQ ID NO:1. In the specification, on page 17, line 1, to page 18, line 5, the applicants disclose methods of determining 90% sequence identity between a nucleic acid and SEQ ID NO:1. Furthermore, given SEQ ID NO:1, one of skill in the art could locate at least 15 contiguous nucleotides within the sequence. It is well established that a patent applicant is entitled to claim his invention broadly, when he describes it sufficiently to meet the requirements of Section 112. See *Utter v. Hiraga*, 6 USPQ2d 1709, 1714 (Fed. Cir. 1988) ("A specification may, within the meaning of 35 U.S.C. §§ 112 para. 1, contain a written description of a broadly claimed invention without describing all species that claim encompasses."). The applicants submit that the specification complies with the requirements for written description, and the Examiner is respectfully requested to withdraw the rejection.

Rejection of Claims 1-45, and 49-51 under 35 U.S.C. §112, First Paragraph

The Examiner has rejected claims 1-45 and 49-51 as allegedly nonenabled. The Examiner acknowledges that the specification is "enabling for nucleotide

sequences encoding SEQ ID NO:2, the promoter activity of bases 1-3202 and a 1.1 kb region downstream from the translational start site of SEQ ID NO:1, a method to produce transgenic plants overexpressing SEQ ID NO:2 displaying some of the phenotypes and changes in biochemical activity listed in the claims, and host plant and bacterial cells, [but] does not reasonably provide enablement for nucleotide sequences encoding polypeptides that differ from SEQ ID NO:2 while retaining its function activity, sequences comprising any type of control element that differ from bases 1-3202 of SEQ ID NO:1, a method to inhibit expression of dwf4 polynucleotides, methods to alter all of the phenotypes in plants or biochemical activities in cells listed in the claims, methods comprising inhibiting dwf4 polynucleotide expression, and all host cells." (Office Action, page 11).

The applicants traverse the rejection. The test for enablement is "whether one skilled in the art could make or use the claimed invention from the disclosure in the patent coupled with information known in the art without undue experimentation." *United States v Telectronics, Inc.* 8 USPQ2d 1217 (Fed. Cir. 1988); *In re Wands,* 8 USPQ2d 1400 (Fed Cir. 1988). Thus, in order to satisfy Section 112 regarding enablement, the specification need only set forth such information as is sufficient to allow one of ordinary skill in the art to make and use the invention. The burden is on the Office to explain its reasons for the rejection and support the rejection with (i) acceptable evidence, or (ii) reasoning which contradicts the applicants' claim: the reasoning must be supported by current literature as a whole and the Office must prove the disclosure requires undue experimentation. *In re Marzocchi*, 439 F.2d 220, 223-24, 169 USPQ 367, 369-70 (CCPA 1971). The Office has failed to provide adequate evidence to support the present rejection. Without such evidence, a rejection under 35 U.S.C. §112, first paragraph for lack of enablement cannot be sustained.

The applicants teach the nucleotide sequence of SEQ ID NO:1 that encodes the polypeptide of SEQ ID NO:2. The specification further teaches that the sequence of DWF4 shares 43% identity with CPD, another cytochrome P450 that acts on a

different substrate. The Examiner states that "it is highly inaccurate to simply assume that all amino acid sequences that have greater than 43% amino acid identity with SEQ ID NO:2 will also share its functional activity." The applicants have not made such an assumption. The Examiner is applying an incorrect test in making the enablement rejection. The test for is not whether one can predict beforehand whether the amino acid sequence would have the desired functional activity. Rather, the test for enablement is whether one of skill in the art can make and use the invention without undue experimentation. Given the disclosure of the present application, only routine experimentation would be required to determine whether the amino acid sequence possesses the desired functional activity. However, in order to expedite the prosecution, the applicants have amended claim 5 to recite a sequence having at least 90% identity to SEQ ID NO:1, complement and reverse complement thereof. In addition, the claim has been amended to recite a sequence comprising at least 15 contiguous nucleotides of SEQ ID NO:1, complement and reverse complement thereof. Thus, the Examiner's concerns regarding 43% sequence identity have veen alleviated.

The Examiner further alleges that the specification does not teach that sequences that differ from bases 1-3202 of SEQ ID NO:1 have any control elements, and cites Kim *et al.* as teaching lack of activity due to changes in a few nucleotides of the nopaline synthase promoter. The applicants disagree. Kim *et al.* investigated the effects of one or more mutations on the activity of the nopaline synthase. The authors created several synthetic oligonucleotides containing point mutations, annealed in TE, ligated into plamids, and cloned into host cells. The activity of the modified promoters was then obtained and compared to the wild-type promoter (Tables 1-4). The activity results were obtained using known screening methods. The reference does not state that unusual techniques were employed in order to determine the activity for a particular change in nucleotide sequence of the promoter. In the present case, the applicants teach dwf4 control elements, and methods for determining whether a sequence has 90% identity to nucleotides 1-3202 of SEQ ID

NO:1. Thus, one of skill in the art could determine, as did Kim *et al.*, the activity of the promoter relative to the wild type using routine experimentation. The Examiner states that retention of promoter activity is unpredictable. However, predictibility is not the test for enablement. The cited reference shows that the effect of changes in the nucleotide sequence of a promoter on the activity of the promoter can be determined without undue experimentation. The Examiner is requested to withdraw the rejection.

The Examiner has rejected the claims as not enabling the alteration of phenotypes related to brassinosteroids, gibberelic acid cytokininins, or auxins. The applicants have amended the claims to remove recitation of these phenotypes.

The Examiner has further rejected the claims to transgenic plants because the phenotype changes or biochemical activity changes of the transgenic plant may be due to inhibition of other genes (page 18). The Examiner states that "it would require undue experimentation by one skilled in the art to use the claimed methods to produce transgenic plants in which only dwf4 gene expression is inhibited and which display the same changes in phenotype and biochemical activity as dwf4 mutant plants, and distinguish the plants from those in which other genes have been affected" (page 18, last sentence). The applicants traverse. The applicants have enabled making transgenic plants that are dwf4 mutants, as acknowledged by the Examiner. In addition, the applicants have enabled determining the phenotype of the transgenic plants. The Examiner states that one could not distinguish phenotypes caused by inhibition of dwf4 versus unintended targets. The claims do not contain an element requiring that other genes remain unaffected. As acknowledged by the Examiner, the specification is enabling for phenotypes associated with dwf4 mutant plants, as claimed.

The Examiner further suggested amending the claims to recite that the host cells are plants or bacterial cells. The applicants thank the Examiner for the suggestion, and have amended claim 25 accordingly.

The rejection of claims 46-48 is made moot by their cancellation.

Thus, in view of the teachings in the specification, undue experimentation would not be required to practice the invention of present claims. The Examiner is respectfully requested to withdraw this rejection.

The Rejection of Claims 1-14 and 20-25 Under 35 U.S.C. §102(a) or 102(b)

The Examiner rejected claims 1-14 and 20-25 as allegedly anticipated by Choe *et al.* The Examiner stated that "Choe *et al.* teach the isolation and nucleotide sequence of instant SEQ ID NO:1 and the locations of the exons and introns of the DWF4 gene comprised within it."

The applicants traverse. The application claims the benefit of U.S. Provisional Applications Serial Nos. 60/119,650 and 60/119,658, both filed on February 11, 1999. Choe *et al.* published on February 25, 1998 (please see the attached email from *The Plant Cell*). The nucleotide sequence disclosed by Choe *et al.*, having the GenBank accession number AF044216, was first released on March 6, 1998 (please see the attached email from GenBank). The reference and the GenBank deposit thus do not meet the requirements for a 102(b) rejection.

The claims were alternatively rejected under 35 U.S.C. §102(a) as anticipated by Choe *et al.* However, the inventors of the present application, AZPIROZ, CHOE and FELDMANN, are coauthors on Choe *et al.* and the relevant portions of Choe *et al.* describe applicants' own work. To evidence this, applicants are submitting a Declaration of Inventors, pursuant to *In re Katz*. The declarations of Choe and Feldmann are included with this response. The declaration of Azpiroz is expected shortly and will be submitted thereupon. Thus, this basis for rejection has been overcome.

Applicants respectfully request withdrawal of the rejection under 35 U.S.C. §102(a) or 102(b).

The Rejection of Claims 1-16, 18-29, 31-35, 38-45, and 49-51 Under 35 U.S.C. §103(a)

The Examiner has rejected claims 1-16, 18-29, 31-35, 38-45, and 49-51under 35 U.S.C. §103(a) as allegedly obvious over Choe *et al.* in view of the applicants' supposed admissions regarding state of prior art.

The applicant traverse the rejection. In order to render claims obvious, the burden is on the Office to establish a *prima facie* case of obviousness for which three basic criteria must be met. First, there must be some suggestion or motivation, either in the references themselves or in the knowledge generally available to one of ordinary skill in the art, to modify the reference. Second, there must be reasonable expectation of success. Finally, the prior art reference must teach or suggest all the claim limitations. The teachings or suggestion to make the claimed combination and the reasonable expectation of success must both be found in the prior art, and not based on applicant's disclosure. *In re Vaeck*, 947 F.2d 488, 20 USPQ2d 1438 (Fed. Cir. 1991). Applicants submit that the cited reference does not disclose all the limitations of the present invention.

Choe *et al.*, as discussed above, in not available as prior art. Thus, a *prima facie* case of obviousness has not been presented by the Office.

In addition, the section in the specification referenced by the Examiner as allegedly an admission by the applicants states: "Techniques for transforming a wide variety of higher plant species are well known and described further below as well as in the technical and scientific literature." Contrary tot he Examiner's assertions, the statement is not an admission by the applicants' on the state of the prior art teachings regarding plant transformation vectors, inducible, constitutive and tissue-specific promoters, and plant transformation techniques, and regeneration of plants from transformed plant cells. The statement refers to the state of the art in light of the teachings of the specification. It is <u>not</u> an admission of prior art.

In the present case, the primary reference, Choe *et al.* is not available as prior art. Therefore, the Office has not presented a *primae facie* case of obviousness, and the rejection should be withdrawn.

Objections

The Examiner has objected to the specification for containing embedded hyperlinks. The applicants have deleted the hyperlinks referenced on page 18 and page 51.

The Examiner has objected to the specification because Figure 3 contains sequences that were not identified by sequence identifiers. The applicants have amended the figure 3 caption to identify the DWF4 polypeptide as Seq ID No.: 2. The Examiner is referred to §2422.03 of the MPEP which states:

> "In those instances in which prior art sequences are only referred to in a given application by name and a publication or accession reference, they need not be included as part of the "Sequence Listing," ..."

The remaining sequences in Figure 3 are art sequences, therefore do not need to be included as part of the "Sequence Listing."

The Examiner objected to Figure 10 because a light gray bar indicating the coding region was absent. The applicants will correct Figure 10, and respond to both the Examiner's and Draftperson's observations upon submission of formal drawings.

The Examiner objected to the specification on page 55 because it incorrectly referred to phylogenetic analysis shown in Figure 6. The applicants have amended the specification to refer to Figure 4 instead, and thank the Examiner for bringing the error to the applicants' attention.

Conclusion

Applicants respectfully submit that the claims define an invention which is novel and nonobvious over the art. Accordingly, a Notice of Allowance is believed in order and is respectfully requested.

If the Examiner notes any further matters which the Examiner believes may be expedited by a telephone interview, the Examiner is requested to contact the undersigned.

Respectfully submitted,

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Appendix A

Marked-up Version

The specification at page 11, line 31, to page 12, line 13, was amended as follows:

Figure 3 depicts alignment of cytochrome P450 proteins that exhibited the most similarity to DWF4 --(Seq ID NO.:2)-- in BLAST searches. GenBank accession numbers are AF044216 (DWF4; CYP90B)--(Seq ID NO.:2)--, X87368 (CPD; CYP90A), U54770 (tomato; CYP85), D64003 (cyanobacteria; CYP120), U32579 (maize; CYP88), U68234 (zebrafish; CYP26), and M13785 (human; CYP3A3X). Dashes indicate gaps introduced to maximize alignment. Domains indicated in Figure 2B are highlighted in a box. Amino acid residues that are conserved >50% between the compared sequences are highlighted by a reverse font, and identical residues between DWF4 and CPD are boxed and italicized. Open triangles are placed under the 100% conserved residues. Closed triangles locate functionally important amino acid residues, for example, threonine (T) at 369, which is thought to bind molecular oxygen, and cysteine (C) at 516, which links to a heme prosthetic group by a thiolate bond. X's indicate mutated residues in *dwf4* alleles. Multiple sequence alignment was performed using PILEUP in the Genetics Computer Group package, and box shading was made possible by the ALSCRIPT package (Barton (1993) *Protein Eng.* 6:37-40). –

The specification at page 17, line 1 to page 18, line 5, was amended follows.

Techniques for determining nucleic acid and amino acid "sequence identity" are known in the art. Typically, such techniques include determining the nucleotide sequence of the mRNA for a gene and/or determining the amino acid sequence encoded thereby, and comparing these sequences to a second nucleotide or amino acid sequence. In general, "identity" refers to an exact nucleotide-to-nucleotide or amino acid-to-amino acid correspondence of two polynucleotides or polypeptide sequences, respectively. Two or more sequences (polynucleotide or amino acid) can be compared by determining their "percent identity." The percent identity of two

sequences, whether nucleic acid or amino acid sequences, is the number of exact matches between two aligned sequences divided by the length of the shorter sequences and multiplied by 100. An approximate alignment for nucleic acid sequences is provided by the local homology algorithm of Smith and Waterman, Advances in Applied Mathematics 2:482-489 (1981). This algorithm can be applied to amino acid sequences by using the scoring matrix developed by Dayhoff, Atlas of Protein Sequences and Structure, M.O. Dayhoff ed., 5 suppl. 3:353-358, National Biomedical Research Foundation, Washington, D.C., USA, and normalized by Gribskov, Nucl. Acids Res. 14(6):6745-6763 (1986). An exemplary implementation of this algorithm to determine percent identity of a sequence is provided by the Genetics Computer Group (Madison, WI) in the "BestFit" utility application. The default parameters for this method are described in the Wisconsin Sequence Analysis Package Program Manual, Version 8 (1995) (available from Genetics Computer Group, Madison, WI). A preferred method of establishing percent identity in the context of the present invention is to use the MPSRCH package of programs copyrighted by the University of Edinburgh, developed by John F. Collins and Shane S. Sturrok, and distributed by IntelliGenetics, Inc. (Mountain View, CA). From this suite of packages the Smith-Waterman algorithm can be employed where default parameters are used for the scoring table (for example, gap open penalty of 12, gap extension penalty of one, and a gap of six). From the data generated the "Match" value reflects "sequence identity." Other suitable programs for calculating the percent identity or similarity between sequences are generally known in the art, for example, another alignment program is BLAST, used with default parameters. For example, BLASTN and BLASTP can be used using the following default parameters: genetic code = standard; filter = none; strand = both; cutoff = 60; expect = 10; Matrix = BLOSUM62; Descriptions = 50 sequences; sort by = HIGH SCORE; Databases = non-redundant, GenBank + EMBL + DDBJ + PDB + GenBank CDS translations + Swiss protein + Spupdate + PIR. [Details of these programs can be found at the following internet address: http://www.ncbi.nlm.gov/cgi-bin/BLAST.]

The specification at page 51, lines 25-30, was amended follows:

Analysis of the complete genomic sequence, starting at the EcoRI site, with the promoter prediction by neural network (NNPP) package [(http://www-hgc.lbl.gov./projects/promoter.html)], indicated that the gene included a putative promoter (TATAT is found in the putative promoter region between nucleotides -143 to -78) and polyadenylation signal sequences (AATAA near a position at 3238 bp and a putative GU-rich signature from 3283 to 3290 bp).

The specification at page 55, line 28, to page 56, line 13, was amended as follows:

Thus, phylogenetic analyses of these seven proteins with cytochrome P450s unique to plants (group A; Durst and Nelson (1995), *supra*) indicate that DWF4 does not cluster with these cytochrome P450s (Figure [6] --4--). Rather, DWF4 clustered with cytochrome P450s from other organisms: cyanobacteria (CYP120), rat (CYP3A2), human (CYP3A3X), and plants (CYP90, CYP85, and CYP88). DWF4 also deviates from the consensus sequence in the group A heme binding domain in that it possesses a PFGGGPRLCAG sequence in which arginine (R) is substituted for proline (P). However, domain A of DWF4, AGHETS, fits the consensus of domain A of group A. These characteristics suggest that DWF4 is a monooxygenase, similar to P450s of group A, that utilizes molecular oxygen as a source of the hydroxyl group, but it mediates some reaction(s) that are not necessarily specific for plants, for instance, steroid hormone biosynthesis, which is a critical event for animals. In fact, the similarity of DWF4 to the rat testosterone 6β-hydroxylase (34%; GenBank accession number 631895) or glucocorticoid-inducible hydroxylase (31%; Molowa et al. 1986; GenBank accession number M13785) supports this idea. Further, the similarity that DWF4 shares with CYP90A and CYP85, 66 and 59%, respectively, is additional proof that it is involved in plant steroid biosynthesis (Bishop et al. 1996 ; Szekeres et al. 1996).

In the Claims

Claims 1-4, 11, 13, 18, and 52-57 have been canceled without prejudice or disclaimer.

Claims 5, 6, 20-22, 24, 28, 29, 34, and 49 have been amended as follows.

5. (Amended) An isolated *dwf4* polynucleotide comprising (i) a sequence having at least [50%] 90% identity to SEQ ID NO:1, [complements] complement and reverse [complements] complement thereof or (ii) a sequence comprising at least about 15 contiguous nucleotides that has at least [50%] 90% identity to SEQ ID NO:1, [complements] complement and reverse [complements] complement thereof.

6. (Amended) The isolated *dwf4* polynucleotide of claim 5 having at least [50%] 90% identity to the DWF4 polypeptide-coding region of SEQ ID NO:1, [complements] complement and reverse [complements] complement thereof.

12. (Amended) A recombinant vector comprising (i) the polynucleotide of claim [5] 6; and (ii) control elements operably linked to said polynucleotide whereby a coding sequence within said polynucleotide can be transcribed and translated in a host cell.

20. (Amended) The isolated polynucleotide of claim 5, wherein the polynucleotide includes a *dwf4* control element comprising a polynucleotide selected from the group consisting of (i) a sequence having at least [50%] 90% identity to nucleotides 1 to 3202 of SEQ ID NO:1; (ii) a fragment of (i) which includes a *dwf4* control element; and (iii) [complements] complement and reverse [complements] complement of (i) or (ii).

21. (Amended) The isolated polynucleotide of claim 5, wherein the polynucleotide includes a *dwf4* control element comprising a polynucleotide selected from the group consisting of (i) a sequence having at least [50%] 90% identity to nucleotides 6111

to 6468 corresponding to the 3' UTR of SEQ ID NO:1; (ii) a fragment of (i) which includes a *dwf4* 3' UTR; and (iii) [complements] complement and reverse [complements] complement of (i) or (ii).

22. (Amended) The isolated polynucleotide of claim 5, [where in] wherein the polynucleotide includes a *dwf4* control element comprising a polynucleotide selected from the group consisting of (i) a sequence having at least [50%] 90% identity to the sequences corresponding to the introns of SEQ ID NO:1; (ii) a fragment of (i) which includes a *dwf4* [intro] intron; and (iii) [complements] complement and reverse [complements] complement of (i) and (ii).

24. (Amended) A recombinant vector comprising[:

(a) the isolated polynucleotide which includes a *dwf4* control element of claim 20; and

(b) a nucleic acid molecule comprising a coding sequence.] an isolated *dwf4* polynucleotide comprising (i) a sequence having at least 90% identity to SEQ ID NO:1, complement and reverse complement thereof or (ii) a sequence comprising at least 15 contiguous nucleotides of SEQ ID NO:1, complement and reverse complement thereof, wherein the polynucleotide includes a *dwf4* control element comprising a polynucleotide selected from the group consisting of (i) a sequence having at least 90% identity to nucleotides 1 to 3202 of SEQ ID NO:1; (ii) a fragment of (i) which includes a *dwf4* control element; and (iii) complement and reverse complement of (i) or (ii).

25. (Amended) A host cell transformed with the recombinant vector of claim 24, wherein the host cell is a plant cell or a bacterial cell.

28. (Amended) A method for producing a transgenic plant having an altered phenotype relative to [the] a wild-type plant comprising the following steps:

introducing at least one polynucleotide of claim 5 into a plant cell; and

producing a transgenic plant from the plant cell, said transgenic plant having an altered phenotype relative to the wild-type plant.

29. (Amended) The method of claim [26] 28, wherein the phenotype is selected from the group consisting of altered cell length, altered periods of flowering, altered branching, altered seed production, altered leaf size, elongated hypocotyls, altered plant height, altered heme-thiolate enzyme activity, altered monooxygenase activity, altered 22α-hydroxylase activity, [regulation of brassinosteriods, regulation of gibberellic acid, regulation of cytokinins, regulation of auxins,] altered resistance to plant pathogens, altered growth at low temperatures, altered growth in dark conditions, and altered sterol composition.

34. (Amended) The method of claim 28, wherein the polynucleotide is operably linked to a promoter selected from the group consisting of a tissue-specific promoter, an inducible promoter [or] and a constitutive promoter.